Top has signature "McGarry", page indicator, "1635", "ENTERED" stamp, handwritten marks.

S. McGarry

1635

ENTERED

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        RAW SEQUENCE LISTING              DATE: 11/29/2000
        PATENT APPLICATION:  US/09/446,402    TIME: 13:41:09

        Input Set : A:\Lucy1.app
        Output Set: N:\CRF3\11292000\I446402.raw

        SEQUENCE LISTING
    4 (1) GENERAL INFORMATION:
    6      (i) APPLICANT: Black Jr., Charles A.
    8     (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ACTIVATING
    9                              GENES OF INTEREST
   11    (iii) NUMBER OF SEQUENCES: 16
   13     (iv) CORRESPONDENCE ADDRESS:
   14          (A) ADDRESSEE: W. Murray Spruill
   15          (B) STREET: 3605 Glenwood Ave. Suite 310
   16          (C) CITY: Raleigh
   17          (D) STATE: NC
   18          (E) COUNTRY: US
   19          (F) ZIP: 27622
   21      (v) COMPUTER READABLE FORM:
   22          (A) MEDIUM TYPE: Floppy disk
   23          (B) COMPUTER: IBM PC compatible
   24          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
   25          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
   27     (vi) CURRENT APPLICATION DATA:
C--> 28          (A) APPLICATION NUMBER: US/09/446,402
C--> 29          (B) FILING DATE: 20-Dec-1999
   30          (C) CLASSIFICATION:
   32   (viii) ATTORNEY/AGENT INFORMATION:
   33          (A) NAME: Spruill, W. Murray
   34          (B) REGISTRATION NUMBER: 32,943
   35          (C) REFERENCE/DOCKET NUMBER: 5722-2
   37     (ix) TELECOMMUNICATION INFORMATION:
   38          (A) TELEPHONE: 919 420 2202
   39          (B) TELEFAX: 919 881 3175
   42 (2) INFORMATION FOR SEQ ID NO: 1:
   44      (i) SEQUENCE CHARACTERISTICS:
   45          (A) LENGTH: 4279 base pairs
   46          (B) TYPE: nucleic acid
   47          (C) STRANDEDNESS: single
   48          (D) TOPOLOGY: linear
   50     (ii) MOLECULE TYPE: other nucleic acid
   51          (A) DESCRIPTION: /desc = "Recombinant molecule
W--> 52                          (Multiple Cloning Site/Kozack sequence/LacZ gene)"
   55     (ix) FEATURE:
   56          (A) NAME/KEY: misc_feature
   57          (B) LOCATION: 1..64
   58          (D) OTHER INFORMATION: /product= "Multiple Cloning Site"
   60     (ix) FEATURE:
   61          (A) NAME/KEY: misc_feature
   62          (B) LOCATION: 65..79
   63          (D) OTHER INFORMATION: /function= "Consensus sequence of
   64 translation initiation"
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 65 /product= "Kozack sequence"
 67      (ix) FEATURE:
 68              (A) NAME/KEY: prim_transcript
 69              (B) LOCATION: 80..4279
 70              (D) OTHER INFORMATION: /gene= "LacZ"
 71 /standard_name= "Beta galactosidase"
 74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 76 TTAATACGAC TCACTATAGG CTAGCCTCGA GAATTCACGC GTGGTACCTC TAGAGTCGAC      60
 78 CCGGGCCGCC GCCACCATGG CGCAGCACCA TGGCCTGAAA TAACCTCTGA AAGAGGAACT     120
 80 TGGTTAGGTA CCTTCTGAGG CGGAAAGAAC CAGCTGTGGA ATGTGTGTCA GTTAGGGTGT     180
 82 GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT CAATTAGTCA     240
 84 GCAACCAGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA GAAGTATGCA AAGCATGCAT     300
 86 CTCAATTAGT CAGCAACCAT AGTCCCGCCC CTAACTCGGC CCATCCCGCC CCTAACTCCG     360
 88 CCCAGTTCCG CCCATTCTCC GCCCCATGGC TGACTAATTT TTTTTATTTA TGCAGAGGCC     420
 90 GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG GAGGCTTTTT TGGAGGCCTA     480
 92 GGCTTTTGCA AAAAGCTTGG GATCTCTATA ATCTCGCGCA ACCTATTTTC CCCTCGAACA     540
 94 CTTTTTAAGC CGTAGATAAA CAGGCTGGGA CACTTCACAT GAGCGAAAAA TACATCGTCA     600
 96 CCTGGGACAT GTTGCAGATC CATGCACGTA AACTCGCAAG CCGACTGATG CCTTCTGAAC     660
 98 AATGGAAAGG CATTATTGCC GTAAGCCGTG GCGGTCTGGT ACCGGTGGGT GAAGACCAGA     720
100 AACAGCACCT CGAACTGAGC CGCGATATTG CCCAGCCGTT CAACGCGCTG TATGGCGAGA     780
102 TCGATCCCGT CGTTTTACAA CGTCGTGACT GGGAAAACCC TGGCGTTACC CAACTTAATC     840
104 GCCTTGCAGC ACATCCCCCT TTCGCCAGCT GGCGTAATAG CGAAGAGGCC CGCACCGATC     900
106 GCCCTTCCCA ACAGTTGCGC AGCCTGAATG GCGAATGGCG CTTTGCCTGG TTTCCGGCAC     960
108 CAGAAGCGGT GCCGGAAAGC TGGCTGGAGT GCGATCTTCC TGAGGCCGAT ACTGTCGTCG    1020
110 TCCCCTCAAA CTGGCAGATG CACGGTTACG ATGCGCCCAT CTACACCAAC GTAACCTATC    1080
112 CCATTACGGT CAATCCGCCG TTTGTTCCCA CGGAGAATCC GACGGGTTGT TACTCGCTCA    1140
114 CATTTAATGT TGATGAAAGC TGGCTACAGG AAGGCCAGAC GCGAATTATT TTTGATGGCG    1200
116 TTAACTCGGC GTTTCATCTG TGGTGCAACG GGCGCTGGGT CGGTTACGGC CAGGACAGTC    1260
118 GTTTGCCGTC TGAATTTGAC CTGAGCGCAT TTTTACGCGC CGGAGAAAAC CGCCTCGCGG    1320
120 TGATGGTGCT GCGTTGGAGT GACGGCAGTT ATCTGGAAGA TCAGGATATG TGGCGGATGA    1380
122 GCGGCATTTT CCGTGACGTC TCGTTGCTGC ATAAACCGAC TACACAAATC AGCGATTTCC    1440
124 ATGTTGCCAC TCGCTTTAAT GATGATTTCA GCCGCGCTGT ACTGGAGGCT GAAGTTCAGA    1500
126 TGTGCGGCGA GTTGCGTGAC TACCTACGGG TAACAGTTTC TTTATGGCAG GGTGAAACGC    1560
128 AGGTCGCCAG CGGCACCGCG CCTTTCGGCG GTGAAATTAT CGATGAGCGT GGTGGTTATG    1620
130 CCGATCGCGT CACACTACGT CTGAACGTCG AAAACCCGAA ACTGTGGAGC GCCGAAATCG    1680
132 CGAATCTCTA TCGTGCGGTG GTTGAACTGC ACACCGCCGA CGGCACGCTG ATTGAAGCAG    1740
134 AAGCCTGCGA TGTCGGTTTC CGCGAGGTGC GGATTGAAAA TGGTCTGCTG CTGCTGAACG    1800
136 GCAAGCCGTT GCTGATTCGA GGCGTTAACC GTCACGAGCA TCATCCTCTG CATGGTCAGG    1860
138 TCATGGATGA GCAGACGATG GTGCAGGATA TCCTGCTGAT GAAGCAGAAC AACTTTAACG    1920
140 CCGTGCGCTG TTCGCATTAT CCGAACCATC CGCTGTGGTA CACGCTGTGC GACCGCTACG    1980
142 GCCTGTATGT GGTGGATGAA GCCAATATTG AAACCCACGG CATGGTGCCA ATGAATCGTC    2040
144 TGACCGATGA TCCGCGCTGG CTACCGGCGA TGAGCGAACG CGTAACGCGA ATGGTGCAGC    2100
146 GCGATCGTAA TCACCCGAGT GTGATCATCT GGTCGCTGGG GAATGAATCA GGCCACGGCG    2160
148 CTAATCACGA CGCGCTGTAT CGCTGGATCA AATCTGTCGA TCCTTCCCGC CCGGTGCAGT    2220
150 ATGAAGGCGG CGGAGCCGAC ACCACGGCCA CCGATATTAT TTGCCCGATG TACGCGCGCG    2280
152 TGGATGAAGA CCAGCCCTTC CCGGCTGTGC CGAAATGGTC CATCAAAAAA TGGCTTTCGC    2340
154 TACCTGGAGA GACGCGCCCG CTGATCCTTT GCGAATACGC CCACGCGATG GGTAACAGTC    2400
156 TTGGCGGTTT CGCTAAATAC TGGCAGGCGT TTCGTCAGTA TCCCCGTTTA CAGGGCGGCT    2460
158 TCGTCTGGGA CTGGGTGGAT CAGTCGCTGA TTAAATATGA TGAAAACGGC AACCCGTGGT    2520
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PATENT APPLICATION: US/09/446,402   TIME: 13:41:09

    Input Set : A:\Lucy1.app
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160 CGGCTTACGG CGGTGATTTT GGCGATACGC CGAACGATCG CCAGTTCTGT ATGAACGGTC   2580
162 TGGTCTTTGC CGACCGCACG CCGCATCCAG CGCTGACGGA AGCAAAACAC CAGCAGCAGT   2640
164 TTTTCCAGTT CCGTTTATCC GGGCAAACCA TCGAAGTGAC CAGCGAATAC CTGTTCCGTC   2700
166 ATAGCGATAA CGAGCTCCTG CACTGGATGG TGGCGCTGGA TGGTAAGCCG CTGGCAAGCG   2760
168 GTGAAGTGCC TCTGGATGTC GCTCCACAAG GTAAACAGTT GATTGAACTG CCTGAACTAC   2820
170 CGCAGCCGGA GAGCGCCGGG CAACTCTGGC TCACAGTACG CGTAGTGCAA CCGAACGCGA   2880
172 CCGCATGGTC AGAAGCCGGG CACATCAGCG CCTGGCAGCA GTGGCGTCTG GCGGAAAACC   2940
174 TCAGTGTGAC GCTCCCCGCC GCGTCCCACG CCATCCCGCA TCTGACCACC AGCGAAATGG   3000
176 ATTTTTGCAT CGAGCTGGGT AATAAGCGTT GGCAATTTAA CCGCCAGTCA GGCTTTCTTT   3060
178 CACAGATGTG GATTGGCGAT AAAAAACAAC TGCTGACGCC GCTGCGCGAT CAGTTCACCC   3120
180 GTGCACCGCT GGATAACGAC ATTGGCGTAA GTGAAGCGAC CCGCATTGAC CCTAACGCCT   3180
182 GGGTCGAACG CTGGAAGGCG GCGGGCCATT ACCAGGCCGA AGCAGCGTTG TTGCAGTGCA   3240
184 CGGCAGATAC ACTTGCTGAT GCGGTGCTGA TTACGACCGC TCACGCGTGG CAGCATCAGG   3300
186 GGAAAACCTT ATTTATCAGC CGGAAAACCT ACCGGATTGA TGGTAGTGGT CAAATGGCGA   3360
188 TTACCGTTGA TGTTGAAGTG GCGAGCGATA CACCGCATCC GGCGCGGATT GGCCTGAACT   3420
190 GCCAGCTGGC GCAGGTAGCA GAGCGGGTAA ACTGGCTCGG ATTAGGGCCG CAAGAAAACT   3480
192 ATCCCGACCG CCTTACTGCC GCCTGTTTTG ACCGCTGGGA TCTGCCATTG TCAGACATGT   3540
194 ATACCCCGTA CGTCTTCCCG AGCGAAAACG GTCTGCGCTG CGGGACGCGC GAATTGAATT   3600
196 ATGGCCACA CCAGTGGCGC GGCGACTTCC AGTTCAACAT CAGCCGCTAC AGTCAACAGC   3660
198 AACTGATGGA AACCAGCCAT CGCCATCTGC TGCACGCGGA AGAAGGCACA TGGCTGAATA   3720
200 TCGACGGTTT CCATATGGGG ATTGGTGGCG ACGACTCCTG GAGCCCGTCA GTATCGGCGG   3780
202 AATTCCAGCT GAGCGCCGGT CGCTACCATT ACCAGTTGGT CTGGTGTCAA AAATAATAAT   3840
204 AACCGGGCAG GCCATGTCTG CCCGTATTTC GCGTAAGGAA ATCCATTATG TACTATTTAA   3900
206 AAAACACAAA CTTTTGGATG TTCGGTTTAT TCTTTTTCTT TTACTTTTTT ATCATGGGAG   3960
208 CCTACTTCCC GTTTTTCCCG ATTTGGCTAC ATGACATCAA CCATATCAGC AAAAGTGATA   4020
210 CGGGTATTAT TTTTGCCGCT ATTTCTCTGT TCTCGCTATT ATTCCAACCG CTGTTTGGTC   4080
212 TGCTTTCTGA CAAACTCGGA ACTTGTTTAT TGCAGCTTAT AATGGTTACA AATAAAGCAA   4140
214 TAGCATCACA AATTTCACAA ATAAAGCATT TTTTTCACTG CATTCTAGTT GTGGTTTGTC   4200
216 CAAACTCATC AATGTATCTT ATCATGTCTG GATCCTCTAG AGTCGACCTG CAGGCATGCA   4260
218 AGCTGGCACT GGCCGTCGT                                                4279
220 (2) INFORMATION FOR SEQ ID NO: 2:
222      (i) SEQUENCE CHARACTERISTICS:
223          (A) LENGTH: 20 base pairs
224          (B) TYPE: nucleic acid
225          (C) STRANDEDNESS: single
226          (D) TOPOLOGY: linear
228     (ii) MOLECULE TYPE: other nucleic acid
229          (A) DESCRIPTION: /desc = "Synthetic oligonucleotide"
234     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
236 GAATACAAAG CTTATGCATG                                                 20
238 (2) INFORMATION FOR SEQ ID NO: 3:
240      (i) SEQUENCE CHARACTERISTICS:
241          (A) LENGTH: 13 base pairs
242          (B) TYPE: nucleic acid
243          (C) STRANDEDNESS: single
244          (D) TOPOLOGY: linear
246     (ii) MOLECULE TYPE: other nucleic acid
247          (A) DESCRIPTION: /desc = "Synthetic oligonucleotide"
252     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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PATENT APPLICATION:  US/09/446,402      TIME: 13:41:09

        Input Set : A:\Lucy1.app
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254 GAATACAAAG CTT                                                    13
256 (2) INFORMATION FOR SEQ ID NO: 4:
258      (i) SEQUENCE CHARACTERISTICS:
259          (A) LENGTH: 20 base pairs
260          (B) TYPE: nucleic acid
261          (C) STRANDEDNESS: single
262          (D) TOPOLOGY: linear
264     (ii) MOLECULE TYPE: other nucleic acid
265          (A) DESCRIPTION: /desc = "Synthetic oligonucleotide"
270     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
272 AAAGCTTATG CATGCGGCCG                                             20
274 (2) INFORMATION FOR SEQ ID NO: 5:
276      (i) SEQUENCE CHARACTERISTICS:
277          (A) LENGTH: 20 base pairs
278          (B) TYPE: nucleic acid
279          (C) STRANDEDNESS: single
280          (D) TOPOLOGY: linear
282     (ii) MOLECULE TYPE: other nucleic acid
283          (A) DESCRIPTION: /desc = "Synthetic oligonucleotide"
288     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
290 CGGCCGCATC TAGAGGGCCC                                             20
292 (2) INFORMATION FOR SEQ ID NO: 6:
294      (i) SEQUENCE CHARACTERISTICS:
295          (A) LENGTH: 25 base pairs
296          (B) TYPE: nucleic acid
297          (C) STRANDEDNESS: single
298          (D) TOPOLOGY: linear
300     (ii) MOLECULE TYPE: other nucleic acid
301          (A) DESCRIPTION: /desc = "Synthetic oligonucleotide"
306     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
308 GCGGCCGCAT CTAGAGGGCC CGGAT                                       25
310 (2) INFORMATION FOR SEQ ID NO: 7:
312      (i) SEQUENCE CHARACTERISTICS:
313          (A) LENGTH: 24 base pairs
314          (B) TYPE: nucleic acid
315          (C) STRANDEDNESS: single
316          (D) TOPOLOGY: linear
318     (ii) MOLECULE TYPE: other nucleic acid
319          (A) DESCRIPTION: /desc = "Synthetic oligonucleotide"
324     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
326 AATACAAAGC TTATGCATGC GGCC                                        24
328 (2) INFORMATION FOR SEQ ID NO: 8:
330      (i) SEQUENCE CHARACTERISTICS:
331          (A) LENGTH: 30 base pairs
332          (B) TYPE: nucleic acid
333          (C) STRANDEDNESS: single
334          (D) TOPOLOGY: linear
336     (ii) MOLECULE TYPE: other nucleic acid
337          (A) DESCRIPTION: /desc = "Synthetic oligonucleotide"
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RAW SEQUENCE LISTING                   DATE: 11/29/2000
PATENT APPLICATION:  US/09/446,402     TIME: 13:41:09

        Input Set : A:\Lucy1.app
        Output Set: N:\CRF3\11292000\I446402.raw
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342     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
344 AATACAAAGC TTATGCATGC GGCCGCATCT                           30
346 (2) INFORMATION FOR SEQ ID NO: 9:
348     (i) SEQUENCE CHARACTERISTICS:
349          (A) LENGTH: 20 base pairs
350          (B) TYPE: nucleic acid
351          (C) STRANDEDNESS: single
352          (D) TOPOLOGY: linear
354     (ii) MOLECULE TYPE: other nucleic acid
355          (A) DESCRIPTION: /desc = "Synthetic oligonucleotide"
360     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
362 CATGCATAAG CTTTGTATTC                                      20
364 (2) INFORMATION FOR SEQ ID NO: 10:
366     (i) SEQUENCE CHARACTERISTICS:
367          (A) LENGTH: 13 base pairs
368          (B) TYPE: nucleic acid
369          (C) STRANDEDNESS: single
370          (D) TOPOLOGY: linear
372     (ii) MOLECULE TYPE: other nucleic acid
373          (A) DESCRIPTION: /desc = "Synthetic oligonucleotide"
378     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
380 AAGCTTTGTA TTC                                             13
382 (2) INFORMATION FOR SEQ ID NO: 11:
384     (i) SEQUENCE CHARACTERISTICS:
385          (A) LENGTH: 20 base pairs
386          (B) TYPE: nucleic acid
387          (C) STRANDEDNESS: single
388          (D) TOPOLOGY: linear
390     (ii) MOLECULE TYPE: other nucleic acid
391          (A) DESCRIPTION: /desc = "Synthetic oligonucleotide"
396     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
398 CGGCCGCATG CATAAGCTTT                                      20
400 (2) INFORMATION FOR SEQ ID NO: 12:
402     (i) SEQUENCE CHARACTERISTICS:
403          (A) LENGTH: 20 base pairs
404          (B) TYPE: nucleic acid
405          (C) STRANDEDNESS: single
406          (D) TOPOLOGY: linear
408     (ii) MOLECULE TYPE: other nucleic acid
409          (A) DESCRIPTION: /desc = "Synthetic oligonucleotide"
414     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
416 GGGCCCTCTA GATGCGGCCG                                      20
418 (2) INFORMATION FOR SEQ ID NO: 13:
420     (i) SEQUENCE CHARACTERISTICS:
421          (A) LENGTH: 25 base pairs
422          (B) TYPE: nucleic acid
423          (C) STRANDEDNESS: single
424          (D) TOPOLOGY: linear
426     (ii) MOLECULE TYPE: other nucleic acid
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VERIFICATION SUMMARY   DATE: 11/29/2000
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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]